

C. Kaufman

Re-run

#12



RAW SEQUENCE LISTING

DATE: 10/03/2002

PATENT APPLICATION: US/09/601,582A

TIME: 15:12:21

Input Set : A:\20052YP.txt

Output Set: N:\CRF4\10032002\I601582A.raw

ENTERED

p.6

4 <110> APPLICANT: Liu, Qingyun  
5 McDonald, Terrence  
6 Bonnert, Timothy P.  
7 Ng, Gordon  
8 Kolakowski, Lee F., Jr.  
9 Clark, Janet  
10 Bonner, Tom I.  
12 <120> TITLE OF INVENTION: NOVEL GABAB RECEPTOR DNA SEQUENCES  
15 <130> FILE REFERENCE: 20052YP  
17 <140> CURRENT APPLICATION NUMBER: 09/601,582A  
18 <141> CURRENT FILING DATE: 2000-12-04  
20 <150> PRIOR APPLICATION NUMBER: PCT/US99/02361  
21 <151> PRIOR FILING DATE: 1999-02-03  
23 <150> PRIOR APPLICATION NUMBER: 60/073,767  
24 <151> PRIOR FILING DATE: 1998-02-05  
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28 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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32 <212> TYPE: DNA  
33 <213> ORGANISM: Homo Sapiens  
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38 gccgcgcgcg ccgcggcgct tctgagccga gccggaaccc tagcccgaga cggagccggg 180  
39 gcccgggcgc gcgccattgc gcgggcgcgc cgggaagacc ttggcgcggg gcggcgggcc 240  
40 gggccaggcc atgcgggcgc agtgagccgc cgcgcgcgc ccgcggcgcg gcatggcttc 300  
41 ccgcgcggagc tcggggcgc ccgggcgcgc gccgcgcgc ccaccgcgc ccgcgcgcct 360  
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46 ctatgacacg gagtgcgaca acgcaaaagg gttgaaagcc ttctacgatg caataaaata 660  
47 cgggcogaac cacttgatgg tgtttggagg cgtctgtcca tccgtcacat ccatcattgc 720  
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49 agccgataag aaaaaatacc cttatttctt tcggaccgtc ccatcagaca atgcggtgaa 840  
50 tccagccatt ctgaagttgc tcaagcacta ccagtggaa cgcgtgggca cgctgacgca 900  
51 agacgttcag aggttctctg aggtgcggaa tgacctgact ggagttctgt atggcgagga 960  
52 cattgagatt tcagacaccg agagcttctc caacgatccc tgtaccagt tcaaaaagct 1020  
53 gaaggggaat gatgtgcgga tcatccttgg ccagtttgac cagaatatgg cagcaaaagt 1080  
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55 ctggtaacgag ccttcttggg gggagcaggt gcacacggaa gccaaactcat cccgctgcct 1200  
56 ccggaagaat ctgcttgctg ccatggaggg ctacattggc gtggatttgc agcccctgag 1260

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57 ctccaagcag atcaagacca tctcaggaaa gactccacag cagtatgaga gagagtacaa 1320
58 caacaagcgg tcaggcgtgg ggcccagcaa gtccacaggg tacgcctacg atggcatctg 1380
59 ggtcatcgcc aagacactgc agagggccat ggagacactg catgccagca gccggcacca 1440
60 gcggatccag gacttcaact acacggacca cacgctgggc aggatcatcc tcaatgccat 1500
61 gaacgagacc aactttcttcg gggtcacggg tcaagttgta ttccggaatg gggagagaat 1560
62 ggggaccatt aaatttactc aatttcaaga cagcaggagg gtgaagggtg gagagtacaa 1620
63 cgctgtggcc gacacactgg agatcatcaa tgacaccatc aggttccaag gatccgaacc 1680
64 accaaaagac aagaccatca tctcggagca gctgcggaag atctccctac ctctctacag 1740
65 catctctctt gccctcacca tctcgggat gatcatggcc agtgcttttc tcttcttcaa 1800
66 catcaagaac cggaatcaga agctcataaa gatgtcgagt ccatacatga acaaccttat 1860
67 catccttgga gggatgctct cctatgcttc catatttctc tttggccttg atggatcctt 1920
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69 ctacacgacc gcttttgggg ccatgtttgc aaagacctgg agagtccacg ccattcttcaa 2040
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91 tcgagcctta tttgtgaagt cttattttct tcacaaagaa gaggaacgga aatgggacgt 3360
92 cttccttaac atctgcaaac aaggaggcgc tgggatatcr aattccacca cactggcggc 3420
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95 &lt;210&gt; SEQ ID NO: 2

96 &lt;211&gt; LENGTH: 941

97 &lt;212&gt; TYPE: PRT

98 &lt;213&gt; ORGANISM: Homo Sapiens

100 &lt;400&gt; SEQUENCE: 2

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102 1 5 10 15
103 Pro Pro Pro Pro Ala Arg Leu Leu Leu Leu Leu Leu Pro Leu Leu
104 20 25 30
105 Leu Pro Leu Ala Pro Gly Ala Trp Gly Trp Ala Arg Gly Ala Pro Arg
106 35 40 45
107 Pro Pro Pro Ser Ser Pro Pro Leu Ser Ile Met Gly Leu Met Pro Leu

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108      50                      55                      60
109 Thr Lys Glu Val Ala Lys Gly Ser Ile Gly Arg Gly Val Leu Pro Ala
110 65                      70                      75                      80
111 Val Glu Leu Ala Ile Glu Gln Ile Arg Asn Glu Ser Leu Leu Arg Pro
112                      85                      90                      95
113 Tyr Phe Leu Asp Leu Arg Leu Tyr Asp Thr Glu Cys Asp Asn Ala Lys
114                      100                      105                      110
115 Gly Leu Lys Ala Phe Tyr Asp Ala Ile Lys Tyr Gly Pro Asn His Leu
116                      115                      120                      125
117 Met Val Phe Gly Gly Val Cys Pro Ser Val Thr Ser Ile Ile Ala Glu
118                      130                      135                      140
119 Ser Leu Gln Gly Trp Asn Leu Val Gln Leu Ser Phe Ala Ala Thr Thr
120 145                      150                      155                      160
121 Pro Val Leu Ala Asp Lys Lys Lys Tyr Pro Tyr Phe Phe Arg Thr Val
122                      165                      170                      175
123 Pro Ser Asp Asn Ala Val Asn Pro Ala Ile Leu Lys Leu Leu Lys His
124                      180                      185                      190
125 Tyr Gln Trp Lys Arg Val Gly Thr Leu Thr Gln Asp Val Gln Arg Phe
126                      195                      200                      205
127 Ser Glu Val Arg Asn Asp Leu Thr Gly Val Leu Tyr Gly Glu Asp Ile
128                      210                      215                      220
129 Glu Ile Ser Asp Thr Glu Ser Phe Ser Asn Asp Pro Cys Thr Ser Val
130 225                      230                      235                      240
131 Lys Lys Leu Lys Gly Asn Asp Val Arg Ile Ile Leu Gly Gln Phe Asp
132                      245                      250                      255
133 Gln Asn Met Ala Ala Lys Val Phe Cys Cys Ala Tyr Glu Glu Asn Met
134                      260                      265                      270
135 Tyr Gly Ser Lys Tyr Gln Trp Ile Ile Pro Gly Trp Tyr Glu Pro Ser
136                      275                      280                      285
137 Trp Trp Glu Gln Val His Thr Glu Ala Asn Ser Ser Arg Cys Leu Arg
138                      290                      295                      300
139 Lys Asn Leu Leu Ala Ala Met Glu Gly Tyr Ile Gly Val Asp Phe Glu
140 305                      310                      315                      320
141 Pro Leu Ser Ser Lys Gln Ile Lys Thr Ile Ser Gly Lys Thr Pro Gln
142                      325                      330                      335
143 Gln Tyr Glu Arg Glu Tyr Asn Asn Lys Arg Ser Gly Val Gly Pro Ser
144                      340                      345                      350
145 Lys Phe His Gly Tyr Ala Tyr Asp Gly Ile Trp Val Ile Ala Lys Thr
146                      355                      360                      365
147 Leu Gln Arg Ala Met Glu Thr Leu His Ala Ser Ser Arg His Gln Arg
148                      370                      375                      380
149 Ile Gln Asp Phe Asn Tyr Thr Asp His Thr Leu Gly Arg Ile Ile Leu
150 385                      390                      395                      400
151 Asn Ala Met Asn Glu Thr Asn Phe Phe Gly Val Thr Gly Gln Val Val
152                      405                      410                      415
153 Phe Arg Asn Gly Glu Arg Met Gly Thr Ile Lys Phe Thr Gln Phe Gln
154                      420                      425                      430
155 Asp Ser Arg Glu Val Lys Val Gly Glu Tyr Asn Ala Val Ala Asp Thr
156                      435                      440                      445

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157 Leu Glu Ile Ile Asn Asp Thr Ile Arg Phe Gln Gly Ser Glu Pro Pro
158      450                      455                      460
159 Lys Asp Lys Thr Ile Ile Leu Glu Gln Leu Arg Lys Ile Ser Leu Pro
160 465                      470                      475                      480
161 Leu Tyr Ser Ile Leu Ser Ala Leu Thr Ile Leu Gly Met Ile Met Ala
162                      485                      490                      495
163 Ser Ala Phe Leu Phe Phe Asn Ile Lys Asn Arg Asn Gln Lys Leu Ile
164                      500                      505                      510
165 Lys Met Ser Ser Pro Tyr Met Asn Asn Leu Ile Ile Leu Gly Gly Met
166                      515                      520                      525
167 Leu Ser Tyr Ala Ser Ile Phe Leu Phe Gly Leu Asp Gly Ser Phe Val
168                      530                      535                      540
169 Ser Glu Lys Thr Phe Glu Thr Leu Cys Thr Val Arg Thr Trp Ile Leu
170 545                      550                      555                      560
171 Thr Val Gly Tyr Thr Thr Ala Phe Gly Ala Met Phe Ala Lys Thr Trp
172                      565                      570                      575
173 Arg Val His Ala Ile Phe Lys Asn Val Lys Met Lys Lys Lys Ile Ile
174                      580                      585                      590
175 Lys Asp Gln Lys Leu Leu Val Ile Val Gly Gly Met Leu Leu Ile Asp
176                      595                      600                      605
177 Leu Cys Ile Leu Ile Cys Trp Gln Ala Val Asp Pro Leu Arg Arg Thr
178                      610                      615                      620
179 Val Glu Lys Tyr Ser Met Glu Pro Asp Pro Ala Gly Arg Asp Ile Ser
180 625                      630                      635                      640
181 Ile Arg Pro Leu Leu Glu His Cys Glu Asn Thr His Met Thr Ile Trp
182                      645                      650                      655
183 Leu Gly Ile Val Tyr Ala Tyr Lys Gly Leu Leu Met Leu Phe Gly Cys
184                      660                      665                      670
185 Phe Leu Ala Trp Glu Thr Arg Asn Val Ser Ile Pro Ala Leu Asn Asp
186                      675                      680                      685
187 Ser Lys Tyr Ile Gly Met Ser Val Tyr Asn Val Gly Ile Met Cys Ile
188                      690                      695                      700
189 Ile Gly Ala Ala Val Ser Phe Leu Thr Arg Asp Gln Pro Asn Val Gln
190 705                      710                      715                      720
191 Phe Cys Ile Val Ala Leu Val Ile Ile Phe Cys Ser Thr Ile Thr Leu
192                      725                      730                      735
193 Cys Leu Val Phe Val Pro Lys Leu Ile Thr Leu Arg Thr Asn Pro Asp
194                      740                      745                      750
195 Ala Ala Thr Gln Asn Arg Arg Phe Gln Phe Thr Gln Asn Gln Lys Lys
196                      755                      760                      765
197 Glu Asp Ser Lys Thr Ser Thr Ser Val Thr Ser Val Asn Gln Ala Ser
198                      770                      775                      780
199 Thr Ser Arg Leu Glu Gly Leu Gln Ser Glu Asn His Arg Leu Arg Met
200 785                      790                      795                      800
201 Lys Ile Thr Glu Leu Asp Lys Asp Leu Glu Glu Val Thr Met Gln Leu
202                      805                      810                      815
203 Gln Asp Thr Pro Glu Lys Thr Thr Tyr Ile Lys Gln Asn His Tyr Gln
204                      820                      825                      830
205 Glu Leu Asn Asp Ile Leu Asn Leu Gly Asn Phe Thr Glu Ser Thr Asp

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206      835      840      845
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208      850      855      860
209 Gln Trp Asn Thr Thr Glu Pro Ser Arg Thr Cys Lys Asp Pro Ile Glu
210 865      870      875      880
211 Asp Ile Asn Ser Pro Glu His Ile Gln Arg Arg Leu Ser Leu Gln Leu
212      885      890      895
213 Pro Ile Leu His His Ala Tyr Leu Pro Ser Ile Gly Gly Val Asp Ala
214      900      905      910
215 Ser Cys Val Ser Pro Cys Val Ser Pro Thr Ala Ser Pro Arg His Arg
216      915      920      925
217 His Val Pro Pro Ser Phe Arg Val Met Val Ser Gly Leu
218      930      935      940
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221 <211> LENGTH: 18
222 <212> TYPE: DNA
223 <213> ORGANISM: Homo Sapiens
225 <400> SEQUENCE: 3
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228 <210> SEQ ID NO: 4
229 <211> LENGTH: 20
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231 <213> ORGANISM: Homo Sapiens
233 <400> SEQUENCE: 4
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236 <210> SEQ ID NO: 5
237 <211> LENGTH: 20
238 <212> TYPE: DNA
239 <213> ORGANISM: Homo Sapiens
241 <400> SEQUENCE: 5
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244 <210> SEQ ID NO: 6
245 <211> LENGTH: 20
246 <212> TYPE: DNA
247 <213> ORGANISM: Homo Sapiens
249 <400> SEQUENCE: 6
250 ggatccatca aggccaaaga
252 <210> SEQ ID NO: 7
253 <211> LENGTH: 19
254 <212> TYPE: DNA
255 <213> ORGANISM: Homo Sapiens
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260 <210> SEQ ID NO: 8
261 <211> LENGTH: 21
262 <212> TYPE: DNA
263 <213> ORGANISM: Homo Sapiens
265 <400> SEQUENCE: 8
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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:23; N Pos. 1992